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TECH CENTER 1600/2908

(1) GENERAL INFORMATION

(i) APPLICANT: Hadlaczky, Gyula  
Szalay, Aladar

(ii) TITLE OF THE INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF  
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES

(iii) NUMBER OF SEQUENCES: 34

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Heller Ehrman White & McAuliffe  
(B) STREET: 4250 Executive Square, 7th Floor  
(C) CITY: La Jolla  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 92037

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/09/724,693  
(B) FILING DATE: 28-NOV-2000

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/835,682  
(B) FILING DATE: 10-APR-1997  
(C) CLASSIFICATION:

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/695,191  
(B) FILING DATE: 07-AUG-1996  
(C) CLASSIFICATION:

(ix) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/682,080  
(B) FILING DATE: 15-JUL-1996  
(C) CLASSIFICATION:

(x) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/629,822  
(B) FILING DATE: 10-APR-1996  
(C) CLASSIFICATION:

(xi) ATTORNEY/AGENT INFORMATION:

(A) NAME: Seidman, Stephanie L  
(B) REGISTRATION NUMBER: 33,779  
(C) REFERENCE/DOCKET NUMBER: 24601-402G

(xii) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 858-450-8403  
(B) TELEFAX: 858-587-5360  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1293 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTTCATCA	TTTTTCANGT	CCTCAAGTGG	ATGTTTCTCA	TTTNCCATGA	TTTTAAGTTT	60
TCTCGCCATA	TTCTCTGGTCC	TACAGTGTGC	ATTTCCTCCAT	TTTNCACGTT	TTNCAGTGAT	120
TTCGTCATTT	TCAAGTCCTC	AAGTGGATGT	TTCTCATTTC	CCATGAATT	CAGTTTCTCN	180
GCCATATTC	ACGTCCTACA	GNNGGACATTT	CTAAATTTC	CACCTTTTC	AGTTTCCCTC	240
GCCATATTC	ACGTCCTAAA	ATGGTGTATT	CTCGTTTNC	GTGATTTCA	GTTTCTCGC	300
CAGATTCCAG	GTCTCTATAAT	GTGCATTCT	CATTNNCAC	GTTTTTCAGT	GATTTCGTCA	360
TTTTTCAAG	TCGGCAAGTG	GATGTTCTC	ATTNNCCATG	ATTTNCAGTT	TTCTTGNAAT	420
ATTCCATGTC	CTACAATGAT	CATTTTAAT	TTTCCACCT	TTCATTTTC	CACGCCATAT	480
TTCATGTCC	AAAGTGTATA	TTTCTCCTT	TCCCGGATT	TCAGTTTCT	CGCCATATTC	540
CAGGTCCTAC	AGTGTGCATT	CCTCATTTT	CACCTTTTC	ACTGATTTCG	TCATTTTICA	600
AGTCGTCAAC	TGGATCTTC	TAATTTCCA	TGATTTTCAG	TTATCTGTC	ATATTCCATG	660
TCCTACAGTG	GACATTCTA	AAATTTCCAA	CTTTTCAAT	TTTCTCGAC	ATATTTGACG	720
TGCTAAAGTG	TGTATTCTT	ATTTCCCGT	ATTTTCAGT	TTCTCGCCAT	ATTCCAGGTC	780
CTAATAGTGT	GCATTTCTCA	TTTTTCACGT	TTTCAGTGA	TTTCGTCATT	TTTTCCAGTT	840
GTCAAGGGGA	TGTTTCTCAT	TTTCCATGAG	TGTCAGTTT	CTTGCTATAT	TCCATGTCCT	900
ACAGTGACAT	TTCTAAATAT	TATACCTTT	TCAGTTTTC	TCACCATATT	TCACGTCCTA	960
AAGTATATAT	TTCTCATTTC	CCCTGATT	CAGTTTCCCT	GCCATATTCC	AGGTCCATACA	1020
GTGTGCATT	CTCATTTTC	ACGTTTTCA	GTAATTCTT	CATTTTTAA	GCCCTCAAAT	1080
GGATGTTCT	CATTTCCAT	GATTTTCAGT	TTTCTTGCCA	TATACCATGT	CCTACAGTGG	1140
ACATTTCTAA	ATTATCCACC	TTTTTCAGTT	TTTCATCGGC	ACATTTCACG	TCCTAAAGTG	1200
TGTATTCTCA	ATTTCAGTG	ATTTTCAGTT	TTCTCGCCAT	ATTCCAGGAC	CTACAGTGTG	1260
CATTTCTCAT	TTTCACGTT	TTTCAGTGA	TTC			1293

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1044 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGGCCTATGG	TGAAAAAGGA	AATATCTTCC	CCTGAAA	AGACAGAAGG	ATTCTCAGAA	60
TCTTATTG	GATGTGCGCC	CCTCAACTAA	CAGTGTGAA	GCTTTCTTT	GATAGAGCAG	120
TTTTGAAACA	CTCTTTTGT	AAAATCTGCA	AGAGGATATT	TGGATAGCTT	TGAGGATTTC	180
CGTTGGAAAC	GGGATTGTCT	TCATATAAAC	CCTAGACAGA	AGCATTCTCA	GAAGCTTCAT	240
TGGGATGTT	CAGTTGAAGT	CACAGTGTG	AACAGTCCC	TTTCATAGAG	CAGGTTGAA	300
ACACTCTTT	TTGTAGTATC	TGGAAGTGG	CATTGGAGC	GATCTCAGGA	CTGCGGTGAA	360
AAAGGAAATA	TCTTCCAATA	AAAGCTAGAT	AGAGGCAATG	TCAGAAACCT	TTTCATGAT	420
GTATCTACTC	AGCTAACAGA	GTTGAACCT	CCTTGAGAG	AGCAGTTTG	AAACACTCTT	480
TTTGTGGAAT	CTGCAAGTGG	ATATTG	AGCTTTGAGG	ATTTCGTTGG	GAAACGGGAT	540
TACATATAAA	AAGCAGACAG	CAGCATTCCC	AGAAACTTCT	TTGTGATGTT	TGCATTCAAG	600
TCACAGAGTT	GAACATTCCC	TTTCATAGAG	CAGGTTGAA	ACACACTTT	TGATGTATCT	660
GGATGTTGGAC	ATTTCAGCG	CTTTCAGGCC	TAAGGTGAAA	AGGAAATATC	TTCCCCTGAA	720
AACTAGACAG	AAGCATTCTC	AGAAACTTAT	TTGTGATGTC	CGCCCTCAAC	TAACAGTGT	780
GAAGCTTCT	TTTGATAGAG	GCAGTTTGAA	AAACTCTTT	TGTGGAATCT	GCAAGTGGAT	840
ATTTGTCTAG	CTTTCAGGAG	TTCTTTGGAA	ACGGGATTAC	ATATAAAAAG	CAGACAGCAG	900

CATTCCCAGA ATCTTGTTG TGATGTTGC ATTCAAGTCA CAGAGTTGAA CATTCCCTT	960
CAGAGAGCAG GTTGAAACAC TCTTTTATA GTATCTGGAT GTGGACATTT GGAGCGCTT	1020
CAGGGGGGAT CCTCTAGAAT TCCT	1044

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGCAGCTGG GGGCTCCAA TCAGGCAGGG GCCCCTTA	ACTCAGATGG GGTGGCCGAG	60
TAGGGGAAGG GGGTCAGGGC TGCATGAGTG GACACAGCTG TAGGACTACC TGGGGGCTGT	120	
GGATCTATGG GGGTGGGAG AAGCCCAGTG ACAGTGCCTA GAAGAGACAA GGTGGCCTGA	180	
GAGGGTCTGA GGAACATAGA GCTGGCCATG TTGGGCCAG GTCTCAAGCA GGAAGTGAGG	240	
AATGGGACAG GCTTGAGGAT ACTCTACTCA GTAGCCAGGA TAGCAAGGAG GGCTTGGGGT	300	
TGCTATCTG GGGTTCAACC CCCCAGTTG AAGGCCCTGG GGGAGATGGT CCCAGGACAT	360	
ATTACAATGG ACACAGGAGG TTGGGACACC TGAGTCACC AAACAAAACC ATGCCAAGAG	420	
AGACCATGAG TAGGGGTGTC CAGTCCAGCC CTCTGACTGA GCTGCATTGT TCAAATCCAA	480	
AGGGGCCCCG CTGCCACCTA GTGGCTGATG GCATCCACAT GACCCCTGGC CACACGCGTT	540	
TAGGGTCTCT GTGAAGACCA AGATCCTGT TACATTGAAC GACTCCTAAA TGAGCAGAGA	600	
TTTCCACCTA TTGCAACAA TCACATAAAA TCCATCCTGG AAAAGCCTG GGGGATGGCA	660	
CTAAGGCTAG GGATAGGGTG GGATGAAGAT TATAGTTACA GTAAGGGTT TAGGGTTAGG	720	
GATCAACGTT GGTTAGGAGT TAGGGATACA GTAGGGTACG GGTAGGGTTA GGGGTTAGGG	780	
TTAGGGGTTA GGGTTAGGGT TAGGGTTAGG GTAGGGTTA GGGGTTAGGG GTTAGGGTTA	840	
GGGTTAGGTT TTGGGGTGGC GTATTTGGT CTTATACGCT GTGTTCCACT GGCAATGAAA	900	
AGAGTTCTTG TTTTCCTTC AGCAATTGTT CAATTTAAA AGAGTTAGC AATTCTAACAA	960	
GATATAGACC AGCTGTGCTA TCTCATTTGTG GTTTCAATT GTAACACAT TGTGGTTTCA	1020	
ATGTGTTTAC TTGCATCTG TAGATCTCT TTGCGTGAGG TGTCTGTTCA GATGTGTGTG	1080	
CATTCTTGN NTTTNGGCTG TTAACTTAT GTTTAGTT TAATAATTT TTATATATTT	1140	
GAAGACAAAT CTTTCTCAGA TGTGTATTTG CAAATATTTC TTCAATATGA GGCTTGCTTT	1200	
TGTCTCTAAC AAGGTCTT CAGAGATAAC TAAATATAA GAAATCCACA CTGTCACTTC	1260	
TTTTGTGTAT ATCTACCTT TGTGTCAATT GTAAAATTC ATTACCAAAC CCAAAGGCAG	1320	
ATAGCTTTTC TTCTATTGTT TCTCTAGAA ATTGTATAG TTTGCATT TTAGTGTAAAG	1380	
GATGATTTTG AGTGATTATT TGTGTAAGTT GTAAAGTTT CGTCTATATC CATATCATT	1440	
CTTATGGTTT CCAATTAATC GTTCCCTCAC TATTTTGAAAGACACAG GATAGTGGGC	1500	
TTTGTAGAG TAGATAGGTA GCTAGACATG AACAGGAGGG GGCCTCCTGG AAAAGGGAAA	1560	
GTCTGGGAAG GCTCACCTGG AGGACCACCA AAAATTCAAA TATTAGTAGC ATCTCTAGTG	1620	
CTGGAGTGGA TGGGCACTTG TCAATTGTTG GTAGGAGGAA AAAGAGGTCC TATGCAGAAA	1680	
GAAACTCCCT AGAACCTCCTC TGAAGATGCC CCAATCATT ACTCTGAAT AAAATGTCA	1740	
GAATATTGCT AGCTACATGC TGATAAGGNN AAAGGGGACA TTCTTAAGTG AAACCTGGCA	1800	
CCATAAGTAC AGATTAGGGC AGAGAAGGAC ATTCAAAAGA GGCAGCGCA GTAGGTACAA	1860	
ACGTGATCGC TGTCACTGTG CCTGGGATGG CGGGAAAGGAG GCTGGTGCCTA GAGTGGATT	1920	
GTATTGATCA CCACACATAT ACCTCAACCA ACAGTGAGGA GGTCCCACAA GCCTAAGTGG	1980	
GGCAAGTGG GGAGCTAAGG CAGTAGCAGG AAAACCAGAC AAAGAAAACA GGTGGAGACT	2040	
TGAGACAGAG GCAGGAATGT GAAGAAATCC AAAATAAAAT TCCCTGCACA GGACTCTTAG	2100	
GCTGTTTAAT GCATCGCTA GTCCCCACTCC TCCCTATT TCTACAATAA ACTCTTACA	2160	
CTGTGTTCTC TTTCAATGAA GTTATCTGCC ATCTTTGTAT TGCCTCTGG TGAAAATGTT	2220	
TCTTCCAAGT TAAACAAGAA CTGGGACATC AGCTCTCCCC AGTAATAGCT CCGTTTCAGT	2280	
TTGAATTTAC AGAACTGATG GGCTTAATAA CTGGCGCTCT GACTTTAGTG GTGCAGGAGG	2340	
CCGTCACACC GGGACCAAGA GTGCCCTGCC TAGTCCCCAT CTGCCCGCAG GTGGCGGCTG	2400	
CCTCGACACT GACAGCAATA GGGTCCGGCA GTGTCCCCAG CTGCCAGCAG GGGCGTACG	2460	
ACGACTACAC TGTGAGCAAG AGGGCCCTGC AG	2492	

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:  
(ix) FEATURE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGAAATTCA TTGGGATGTT TCAGTTGA

28

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:  
(ix) FEATURE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAAAGTCCC CCCTAGGAGA TCTTAAGGA

29

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 47 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:  
(ix) FEATURE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAACGCTC TCGCACC

47

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA  
(iii) HYPOTHETICAL: NO

- (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE:
  - (vi) ORIGINAL SOURCE:
  - (ix) FEATURE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGATTAAAT TAATTAAGCC CGGGC

25

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 27 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Genomic DNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE:
  - (vi) ORIGINAL SOURCE:
  - (ix) FEATURE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAAATTTAAT TAATTCGGGC CCGTCGA

27

*cont*  
(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 69 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Genomic DNA
  - (D) OTHER INFORMATION IL-2 signal sequence
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT  
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu

48

GTC ACA AAC AGT GCA CCT ACT  
Val Thr Asn Ser Ala Pro Thr

69

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 945 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...942
  - (D) OTHER INFORMATION: Renilla Reiniformis Luciferase

(x) PUBLICATION INFORMATION:

(H) Document Number: 5,418,155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGC TTA AAG ATG ACT TCG AAA GTT TAT GAT CCA GAA CAA AGG AAA CGG Ser Leu Lys Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg 1 5 10 15	48
ATG ATA ACT GGT CCG CAG TGG TGG GCC AGA TGT AAA CAA ATG AAT GTT Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val 20 25 30	96
CTT GAT TCA TTT ATT AAT TAT TAT GAT TCA GAA AAA CAT GCA GAA AAT Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn 35 40 45	144
GCT GTT ATT TTT TTA CAT GGT AAC GCG GCC TCT TCT TAT TTA TGG CGA Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg 50 55 60	192
CAT GTT GTG CCA CAT ATT GAG CCA GTA GCG CGG TGT ATT ATA CCA GAT His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp 65 70 75 80	240
CTT ATT GGT ATG GGC AAA TCA GGC AAA TCT GGT AAT GGT TCT TAT AGG Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg 85 90 95	288
TTA CTT GAT CAT TAC AAA TAT CTT ACT GCA TGG TTG AAC TTC TTA ATT Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Leu Asn Phe Leu Ile 100 105 110	336
TAC CAA AGA AGA TCA TTT TTT GTC GGC CAT GAT TGG GGT GCT TGT TTG Tyr Gln Arg Arg Ser Phe Phe Val Gly His Asp Trp Gly Ala Cys Leu 115 120 125	384
GCA TTT CAT TAT AGC TAT GAG CAT CAA GAT AAG ATC AAA GCA ATA GTT Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val 130 135 140	432
CAC GCT GAA AGT GTA GTA GAT GTG ATT GAA TCA TGG GAT GAA TGG CCT His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro 145 150 155 160	480
GAT ATT GAA GAA GAT ATT GCG TTG ATC AAA TCT GAA GAA GGA GAA AAA Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys 165 170 175	528
ATG GTT TTG GAG AAT AAC TTC TTC GTG GAA ACC ATG TTG CCA TCA AAA Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys 180 185 190	576
ATC ATG AGA AAG TTA GAA CCA GAA GAA TTT GCA GCA TAT CTT GAA CCA Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro 195 200 205	624
TTC AAA GAG AAA GGT GAA GTT CGT CGT CCA ACA TTA TCA TGG CCT CGT Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg 210 215 220	672
GAA ATC CCG TTA GTA AAA GGT GGT AAA CCT GAC GTT GTA CAA ATT GTT Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val 225 230 235 240	720
AGG AAT TAT AAT GCT TAT CTA CGT GCA AGT GAT GAT TTA CCA AAA ATG	768

Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met		
245	250	255
TTT ATT GAA TCG GAT CCA GGA TTC TTT TCC AAT GCT ATT GTT GAA GGC		816
Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly		
260	265	270
GCC AAG AAG TTT CCT AAT ACT GAA TTT GTC AAA GTA AAA GGT CTT CAT		864
Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His		
275	280	285
TTT TCG CAA GAA GAT GCA CCT GAT GAA ATG GGA AAA TAT ATC AAA TCG		912
Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser		
290	295	300
TTC GTT GAG CGA GTT CTC AAA AAT GAA CAA TAA		945
Phe Val Glu Arg Val Leu Lys Asn Glu Gln		
305	310	

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTGAATTCA TGTACAGGAT GCAAATCCTG 30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGAATTCA GTAGGTGCAC TGTTTGTAC 30

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1434 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO

- (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE:
  - (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	AGAGCAGCGT	TGGGGGATAAA	60
TGTCGACATT	TCCACTCCC	ATGACGGTGA	TGTATAATGC	TCAAGTATT	TCCTGCTTT	120
TTACCACTAA	CTAGGAAC	GTGTTGGCCT	TAATTCA	AGCCTTGGCT	CTGTCTGGAC	180
AGGTCCAGAC	GACTGACACC	ATTAACACTT	TGTCA	AGTGA	TCATAGATG	240
AACAGGCC	AGCTAATGTC	AAGATACAGA	GAGGTCTCAT	GCTGGTTAAT	CAACTCATAG	300
ATCTTGTC	GATACAAC	GATGTATTAT	GACAAATAAC	TCAGCAGGG	TGTGAACAAA	360
AGTTTCCGGG	ATTGTGTGTT	ATTTCCATT	AGTATGTTAA	ATTTACTAGG	ACAGCTAATT	420
TGTCAAAAG	TCTTTTTCAG	TATATGTTAC	AGAATTGGAT	GGCTGA	AAACAGATCC	480
TTCGGGAATT	GAGACTTCAG	GTCAACTCCA	CGCGCTTGG	CCTGTCGCTG	ACCAAAGGAT	540
TACCCAA	TGATCCTCA	GCATTTCTT	TCTTAA	ATGGGTGGG	TIAATATTAT	600
TTGGAGATAC	ACTTGCTGT	GGATTAGTGT	TGCTTCTT	ATTGGTCTGT	AAGCTTAAGG	660
CCCAAAC	GAGAGACAAG	GTGTTATTG	CCCAGGCGCT	TGCAGGACTA	GAACATGGAG	720
CTTCCCCTGA	TATATGGTTA	TCTATGCTTA	GGCAATAGGT	CGCTGCCAC	TCAGCTCTTA	780
TATCCCACGA	GGCTAGTCTC	ATTGTACGGG	ATAGAGTGA	TGTGCTTCAG	CAGCCCAGA	840
GAGTTGCAAG	GCTAAGCACT	GCAATGGAAA	GGCTCTGCGG	CATATATGTG	CCTATTCTAG	900
GGGGACATGT	CATCTTCAT	GAAGGTTCA	TGCTCTAGTT	CCCTTCCCC	AGGCAAAACG	960
ACACGGGAGC	AGGTCAAGG	TGCTCTGGGT	AAAAGCCTGT	GAGCCTGGG	GCTAACCTG	1020
TACATGGCTC	CTTACCTAC	ACACTGGG	TTGACCTCT	ATCTCACTC	TCATTAATAT	1080
GGGTGGCTA	TTTGTCTTA	TTAAAGGAA	AGGGGAGAT	GTTGGGAGG	GCGCCCCACAT	1140
TCGCCGTTAC	AAGATGGCGC	TGACAGCTGT	GTCTAAGTG	GTAAACAAAT	AATCTGCGCA	1200
TGTGCGGAGG	GTGGTTCTC	ACTCCATGTG	CTCTGCC	CCCGTGACGT	CAACTCGGCC	1260
GATGGGCTGC	AGCCAATCAG	GGAGTGACAC	GTCCTAGGCG	AAGGAGAATT	CTCCTTAATA	1320
GGGACGGGGT	TTCGTTCTC	CTCTCTCT	TGCTTCTCT	TCTTGCTTT	TCGCTCTCTT	1380
GCTTCCCGTA	AAGTGATAAT	GATTATCATC	TACATATCAC	AACGTGCGTG	GAGG	1434

*R. J. Smith*  
(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1400 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Genomic DNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE:
  - (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	AGAGCAGCGT	TGGGGGATAAA	60
TGTCGACATT	TCCACTCCC	ATGACGGTGA	TGTATAATGC	TCAAGTATT	TCCTGCTTT	120
TTACCACTAA	CTAGGAAC	GTGTTGGCCT	TAATTCA	AGCCTTGGCT	CTGTCTGGAC	180
AGGTCCAGAT	ACAAC	GTATTATGAC	AAATAACTCA	GCAGGGATGT	GAACAAAAGT	240
TTCCGGGATT	CGCGTGTATT	TCCATCCAGT	ATGTTAAAT	TACTAGGGCA	GCTAATTGTT	300
CAAAAGTCT	TTTCAGTAT	ATGTTACAGA	ATTGGATGGC	TGAATTGAA	CAGATCCTC	360
GGGAATTGAG	ACTTCAGTC	AACTCCACGC	GCTTGGACCT	GTCTTGACC	AAAGGATTAC	420
CCAATTGGAT	CTCCTCAGCA	TTTTCTTCT	TTAA	GGTGGGATT	ATATTATTG	480
GAGATACACT	TTGCTGTGGA	TTAGTGTG	TTCTTGATT	GGTCTGTAAG	CTTAAGGCC	540
AAACTAGGAG	AGACAAGGTG	GTTATTGCC	AGGCGCTTG	AGGACTAGAA	CATGGAGCTT	600
CCCCTGATAT	ATCTATGCTT	AGGCAATAGG	TCGCTGGCA	CTCAGCTCTT	ATATCCCATG	660
AGGCTAGTCT	CATTGACCGG	GATAGAGTGA	GTGTGCTTC	GCAGCCCGAG	AGAGTTGCAC	720
GGCTAACGAC	TGCAATGGAA	AGGCTCTGCG	GCATATATGA	GCCTATTCTA	GGGAGACATG	780
TCATCTTCA	AGAAGGTTGA	GTGTCCAAGT	GTCTTCC	CAGGCAAAAC	GACACGGGAG	840
CAGGTCAAGG	TTGCTCTGGG	TAAAAGCCTG	TGAGCCTAAG	AGCTAATCCT	GTACATGGCT	900
CCTTACCTA	CACACTGGGG	ATTTGACCTC	TATCTCCACT	CTCATTAATA	TGGGTGGCCT	960
ATTGCTCTT	ATTAAGGAA	AAGGGGAGA	TGTTGGGAGC	CGCGCCAC	TTCGCCGTTA	1020
CAAGATGGCG	CTGACAGCTG	TGTTCTAAGT	GGTAAACAA	TAATCTGCG	ATGCGCCGAG	1080
GGTGGTTCTT	CACTCCATGT	GCTCTGCC	CCCCGTGACG	TCAACTCGGC	CGATGGGCTG	1140
CAGTCATCA	GGGAGTGACA	CGTCCTAGGC	GAAGGAAAT	TCTCCTTAAT	AGGGACGGGG	1200

TTTCGTTTC	TCTCTCTT	GCTTCGCTCT	CTCTTGCTTC	TTGCTCTCTT	TTCCTGAAGA	1260
TGTAAGATA	AAGCTTGCC	GCAGAAAGATT	CTGGTCTGTG	GTGTTCTTCC	TGGCCGGTCG	1320
TGAGAACGCG	TCTAATAACA	ATTGGTGCCG	AAACCCGGGT	GATAATGATT	ATCATCTACA	1380
TATCACAACG	TGCGTGGAGG					1400

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1369 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	ACTTTACGGG	TCCTTCACT	60
ACAACCTGCCA	CGAGGCCCG	TGCTCTGGTA	ATAGATCTT	GCTGAAAAGG	CACACACATG	120
ACACATTACT	CAAGGTGGGC	TCATCTGAGC	TGAGATTCA	GCTTAATATG	AATCTTGCCA	180
ATTGTGTGAA	ATCATAAATC	TTCAAAGTGA	CACTCATTGC	CAGACACAGG	TGCCCACCTT	240
TGGCATAATA	AAACAAACACA	AATTATCTAT	TATATAAAGG	GTGTTAGAAG	ATGCTTTAGA	300
ATACAAATAA	ATCATGGTAG	ATAACAGTAA	GTGAGAGCT	TAAATTAAAT	AAAGTGATAT	360
ACCTAATAA	AATTAAATTA	AGAAGGTGTG	AATATACTAC	AGTAGGTTAA	TTATTTCAATT	420
AATTATTTT	CTTCTTAAT	CCTTATAAT	GTTTCTGCT	ATTGTCAATT	GCACATCCAT	480
ATGTTCAATT	CTTCACTGT	ATGAAGAAAT	GTAGTAAATA	TACTTCCGA	ACAAGTTGTA	540
TCAAATATGT	TACACTTGAT	TCCGTGTGTT	ACTTATCATT	TTATTATTAT	ATTGATTGCA	600
TTCCCTCGTT	ACTTGATATT	ATTACAAGGT	ACATATTAT	TCTCTCAGAT	CTTCATTATA	660
CTCTAACCAT	TTTATAACAT	ACTTTATTTA	TTCATTTCTT	ATGTGTGCTG	TGAGGCACAA	720
ATGCCAGAGA	GAACCTTGAGC	AGATAAGAGG	AAACATTGCA	AGAGTCAGTT	ACCTCCTGCT	780
GTTCCTTGG	AACTCAGGAT	CAAATTCAAG	TTGTCAGGCT	TGGCAGCATG	CACTTTTAC	840
CAGTGCCTCC	ATCTTGCTAG	CCCTGAACAT	CAAGCTTGC	AGACAGACAG	GCTACACTAA	900
GTGAACTGGT	CATTACACAGC	ATGCATGGTG	ATTTATTGTT	ACTTTCTATT	CCATGCCTT	960
ACTATTTCTA	CTAGGTGCTA	GCTAGTACTG	TATTCGAGA	TAGAAGTTAC	TGAAAGAAAA	1020
TTACATTGTT	TTCTATAGAT	CCTTGATACT	CTTTCAGCAG	ATATAGAGTT	TTAACAGGT	1080
CCTAGACCCCT	TTCTTCACTC	TTATTAAATA	CTAAGTACAA	ATTAAGTTA	TCCAAAACAG	1140
TACGGATGTT	GATTGGTGC	AGTTCTACTA	TGATAATAGT	CTAGCTTCAT	AAATCTGACA	1200
CACTTATTGG	GAATGTTTT	GTAAATAAAA	GATTCAAGGTG	TTACTCTAGG	TCAAGAGAAAT	1260
ATTAACACATC	AGTCCCAAAT	TACAAACTTC	AATAAAAGAT	TTGACTCTCC	AGTGGTGGCA	1320
ATATAAAGTG	ATAATGATTA	TCATCTACAT	ATCACAACGT	CGCGTGGAGG		1369

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22118 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCCCT	ATCCCTAAC	CAGATTGGTG	GAATAACTTG	GTATAGATGT	TTGTGCATTA	60
AAAACCCCTGT	AGGATCTTCA	CTCTAGGTCA	CTGTTCAGCA	CTGGAACCTG	AATTGTGGCC	120
CTGAGTGATA	GGTCCCTGGGA	CATATGCAGT	TCTGCACAGA	CAGACAGACA	GACAGACAGA	180
CAGACAGACA	GACAGACGTT	ACAAACAAAC	ACGTTGAGCC	GTGTGCCAAC	ACACACACAA	240
ACACCACTCT	GGCCATAATT	ATTGAGGACG	TTGATTATT	ATTCTGTGTT	TGTGAGTCTG	300
TCTGTCTGTC	TGTCTGTCTG	TCTGTCTGTC	TATCAAACCA	AAAGAAACCA	AACAATTATG	360

CCTGCCTGCC	TGCCTGCCTG	CCTACACAGA	GAAATGATT	CTTCAATCAA	TCTAAAACGA	420
CCTCCTAAGT	TTGCCTTTT	TCTCTTCCT	TATCTTTTC	TTTTTCTTT	TCTTCTTCCT	480
TCCTCCCTC	CTTCCCTCCT	TCCTCCTT	CTTCTTCTC	TTCTTCTTT	CTTACTTCT	540
TTCTTCTCT	CTTACATTTA	TTCTTTCAT	ACATAGTTTC	TTAGTGTAAAG	CATCCCTGAC	600
TGTCTTGAAAG	ACACTTTGTA	GGCCTCAATC	CTGTAAGAGC	CTTCCCTCTG	TTTCAAAATG	660
CTGGCATGAA	TGTGTACCT	CACTATGACC	AGCTTAGTCT	TCAAGTCTGA	GTAACTGGAA	720
AGGAGTTCCA	AGAAGACTGG	TTATATTTT	CATTTATTAA	TGCAATTAA	TTAAAATTAA	780
ATTCACCAA	AAGAATTAG	ACTGACCAAT	TCAGAGTCTG	CCGTTAAAAA	GCATAAGGAA	840
AAAGTAGGGAG	AAAACAGTGA	GGCTGCTGT	GGATGGTCGA	GGCTGCTTTA	GGGAGCCTCG	900
TCACCATCT	GCACTTGCAA	ACCGGGCCAC	TAGAACCCGG	TGAAGGGAGA	AACCAAAGCG	960
ACCTGGAAAC	AATAGGTAC	ATGAAGGCCA	GCCACCTCCA	TCTTGTGTG	CGGGAGTCA	1020
GTTAGCAGAC	AAGATGGCTG	CCATGCACAT	GTGTCCTTC	AGCTTGGTGA	GGTCAAAGTA	1080
CAACCGAGTC	ACAGAACAAAG	GAAGTATACA	CAGTGAGTTC	CAGGTCAGCC	AGAGTTTACA	1140
CAGAGAACAC	ACATCTTGAA	AAAAACAAAAA	AAATAAATTAA	AATAAATATA	ATTTAAAAT	1200
TTAAAATAG	CCGGGAGTGA	TGGCGCATGT	CTTAATATCCC	AGCTCTCTTC	AGGCAGAGAT	1260
GGGAGGAGTT	CTGAGTTGCA	GGCCAGCTG	GTCTGCAAAG	TGAGITCCAG	GACAGTCAGG	1320
GCTATACAGA	GAACCCCTGT	CTTGAAAAC	AAACTAAATT	AAACTAAACT	AAACTAAAAA	1380
AAATAAAAT	AAAATTTTA	AAGAATTAA	AAAAACTACA	GAAATCAAAC	ATAAGCCCCAC	1440
GAGATGGCAA	GTAACTGCAA	TCATAGCAGA	AAATTATAC	ACACACACAC	ACACAGACTC	1500
TGTCATAAAA	TCCAATGTGC	CTTCATGATG	ATCAAATTTC	GATAGTCAGT	ATAACTAGAA	1560
GAATCATATG	TCTGAAAATA	AAAGCCAGAA	CCCTTCTGC	TTTTGTTTTC	TTTTGCCCA	1620
AGATAGGGTT	TCTCTCAGTG	TATCCCTGGC	ATCCCTGCCT	GGAACTTCCT	TTGTAGGTTT	1680
GGTAGCCTCA	AACTCAGAGA	GGTCCTCTCT	GCCTGCCTGC	CTGCCTGCCT	GCCTGCCTGC	1740
CTGCCTGCCT	GCCTGCCTCA	CTTCTCTGC	CACCCACACA	ACCGAGTCGA	ACCTAGGATC	1800
TTTATTCTTCT	TCTCTTCTC	TCTTCTTCT	TTCTTCTTCT	TTCTTCTTCT	TTCTTCTTCT	1860
CTTCTTTCT	TTCTTATTCA	ATTAGTTTC	AATGTAAGTG	TGTGTTGTG	CTCTATCTGC	1920
TGCTATAGG	CCTGCTTGCC	AGGAGAGGGC	AACAGAACCT	AGGAGAAACC	ACCATGCAGC	1980
TCCTGAGAAT	AAGTAAAAAA	ACAACAAAAA	AAGGAAATT	TAATCACATA	GAATGTAGAT	2040
ATATGCCGAG	GCTGTCAGAG	TGCTTTTAA	GGCTTAGTGT	AAGTAATGAA	AATTGTTGTG	2100
TGTCTTTAT	CCAAACACAG	AAGAGAGGTG	GCTCGGCCCTG	CATGTCCTGTT	GTCTGCATGT	2160
AGACCAGGCT	GGCCTTGAAAC	ACATTAATCT	GTCTGCCTCT	GCTTCCCTAA	TGCTGCGATT	2220
AAAGGCATGT	GCCACCACTG	CCCGGACTGA	TTTCTTCTTT	TTTTTTTTT	TGGAAAATAC	2280
CTTTCTTCT	TTTCTCTCT	CTCTTCTTC	CTTCTTCTCT	TTCTTCTTAT	TCTTTTTTTC	2340
TTTCTTTTTT	CTTTTTTTT	TTTTTTTTAA	AATTGCTTA	AGGTTAAAGG	TGTGCTCCAC	2400
AATTGCCCA	GCTCTGCTCT	AATTCTCTT	AAAAAAAC	AAACAAAAAA	AAAACCAAA	2460
CAGTATGTAT	GTATGTATAT	TTAGAAGAAA	TACTAATCCA	TTAATAACTC	TTTTTCTTA	2520
AAATTCACTG	CATTCTTGT	CCACAAAGTG	AGTTCAGGAGA	CTTACCCAGAG	AAACCCCTGTG	2580
TTCAAATTTC	TGTGTTCAAG	GTCACCCCTGG	CTTACAAAGT	GAGTTCCAAG	TCCGATAGGG	2640
CTACACAGAA	AAACCATATC	TCAGAAAAAA	AAAAGTTCC	AAACACACAC	ACACACACAC	2700
ACACACACAC	ACACACACAC	ACACACACAC	ACACACACAG	CGGCCGCGGG	CGATGAGGGGG	2760
AAGTCGTGCC	AAAATAAAAT	ATTTTCTGG	CCAAAGTGAAG	AGCAAAATCAC	TATGAAGAGG	2820
TACTCTCTAGA	AAAATAAAAT	ACAAACGGGC	TTTTAATCA	TTCCAGCACT	TTTTTAATT	2880
AACTCTGAAT	TTAGTCTTGG	AAAAGGGGGC	GGGTGTGGGT	GAGTGAAGGC	GAGCGAGCAG	2940
ACGGGCGGGC	GGGGGGGTGA	GTGGCCCGCG	GGGGTGGCAG	CGAGCACCG	AAAACAACAA	3000
ACCCCAAGCG	GTAGAGTGT	TTAAAAATGA	GACCTAAATG	TGGTGAACAG	GAGGTGCGCCG	3060
CCACCCCTCT	CTTCCACTGC	TTAGATGCTC	CCTTCCCTT	ACTGTGCTCC	CTTCCCCCTAA	3120
CTGTGCCTAA	CTGTGCCTGT	TCCCCTCACCC	CGCTGATTCG	CCAGCGACGT	ACTTTGACTT	3180
CAAGAACGAT	TTGCCTGTT	TTCACCGCTC	CCTGTACATAC	TTTCGTTTTT	GGGTGCCCGA	3240
GTCTAGCCCG	TTCGCTATGT	TCGGGGGGGA	CGATGGGGAC	CGTTTGTGCC	ACTCGGGAGA	3300
AGTGGTGGGT	GGGTACGCTG	CTCCGTCGTG	CGTGCCTGAG	TGCCGGAACC	TGAGCTCGGG	3360
AGACCCCTCCG	GAGAGACAGA	ATGAGTGTAGT	GAATGTGGCG	GCGCGTGACG	GATCTGTATT	3420
GGTTTGTATG	GTGTGATCGAG	ACCATTGTCG	GGCGCACACCT	AGTGGTGACA	AGTTTCGGGA	3480
ACGCTCCAGG	CCTCTCAGGT	TGGTGACACA	GGAGAGGGAA	GTGCCTGTGG	TGAGGCAGACC	3540
AGGGTGACAG	GAGGCCGGC	AAGCAGGGCG	GAGCGTCTCG	GAGATGGTGT	CCTGTTTAAG	3600
GACGGTCTCT	AAACAGGAGG	TCGTACAGGG	AGATGGCCAA	AGCAGACCGA	GTGCTGTAC	3660
GCCCTTTGG	AAAAATGCT	AGGGTTGGTG	GCAACGTTAC	TAGGTGACCC	AGAAGGCTTA	3720
AGTCCTACCC	CCCCCCCCCT	TTTTTTTTT	TTTCTCCAG	AAGCCCTCTC	TTGTCCCCGT	3780
CACCGGGGGC	ACCGTACATC	TGAGGCCAG	AGGACGCGAT	GGGCCCGGCT	TCCAAGCCGG	3840
TGTGGCTCGG	CCAGCTGGCG	CTTCGGGTCT	TTTTTTTTT	TTTTTTTTT	TTTCCTCCA	3900
GAAGCCTTGT	CTGTCGCTGT	CACCGGGGGC	GCTGTACTTC	TGAGGCCAG	AGGACGCGAT	3960
GGGCCCCGGC	TTCCAAGGCCG	GTGTGGCTCG	GCCAGCTGGA	GCTTCGGGTC	TTTTTTTTTT	4020
TTTTTTTTT	TTTTTTCTC	CAGAAGCCTT	GTCTGTCGCT	GTCACCGGGGG	GCGCTGTACT	4080
TCTGAGGCGC	AGAGGACGCG	ATGGGTCCGC	TTCCAAGGCCG	ATGTGGCGGG	CCCAGCTGGA	4140
GCTTCGGGGT	TTTTTTTTTC	CTCCAGAACG	CCTCTCTTGT	CCCCGTCA	GGGGGCGCTG	4200
TACTTCTGAG	GCCGAGAGGA	CGTGATGGC	CCGGGTTCCA	GGCGGATGTC	GCCCGGTCA	4260
CTGGAGCTT	GGATCTTTT	TTTTTTTTT	CCTCCAGAACG	CCCTCTCTT	CCCCGTCA	4320
CGGGGGCACC	TTACATCTGA	GGGCGAGAGG	ACGTGATGGG	TCCGGCTTCC	AAGCCGATGT	4380

GGCGGGGCCA	GCTGGAGCTT	CGGGTTTTT	TTTTTCCTC	CAGAACCCCT	CTCTTGCCC	4440
CGTCACCGGG	GGCGCTGTAC	TTCTGAGGCC	GAGAGGACGT	GATGGGCCCG	GGTTCAGGC	4500
GGATGTCGCC	CGGTCACTG	GAGCTTGGA	TCATTTTTT	TTTCCCTCC	AGAACCCCTC	4560
TCTTGTCCCC	GTCACCAGGG	GCACCGTACA	TCTGAGGCCG	AGAGGACACG	ATGGGCCTGT	4620
CTTCCAAGCC	GATGTGGCC	GGCCAGCTGG	AGCTTCGGGT	CTTTTTTTT	TTTTTCCTC	4680
CAGAACGCTT	GTCACCGGG	GCGCTGTACT	TCTGAGGCCG	AGAGGACGCG	4740	
ATGGGCCCGG	CTTCAAGCC	GGTGTGGCTC	GGCCAGCTGG	AGCTTCGGGT	CTTTTTTTT	4800
TTTTTTTTT	TTCTCAGA	AACCTTGCT	GTCCTGTCA	CCCAGGGCGC	TTGTACTTCT	4860
GATGCGAGA	GGACCGCATG	GGCCCGCTT	CCAGGCCAT	GTGGCCCGGT	CAGCTGGAGC	4920
TTTGGATCTT	TTTTTTTTT	TTTCCCTCA	GAAGCCCTCT	CTTGTCCCCG	TCACCGGGG	4980
CACCTTACAT	CTGAGGCCTA	GAGGACACGA	TGGGCCCGGG	TTCCAGGCCG	ATGTGGCCCG	5040
GTCAGCTGGA	GCTTTGGATC	TTTTTTTTT	TTTCTTCCA	GAAGCCCTCT	TGTCCCCGTC	5100
ACCGGTGGCA	CTGTACATCT	GAGGCAGGAGA	GGACATTATG	GGCCCGGCTT	CCAATCCGAT	5160
GTGGCCCGGT	CAGCTGGAGC	TTTGGATCTT	ATTTTTTTT	TAATTTTTTC	TTCCAGAACG	5220
CCTCTTGTCC	CTGTCACCGG	TGGCACCGTA	CATCTGAGGC	CGAGAGGACA	TTATGGGCC	5280
GGCTTCCAGG	CCGATGTGGC	CCGGTCACTG	GGAGCTTTGG	ATCTTTTTT	TTTTTTTCT	5340
TTTTCTTCC	AGAACCCCTC	TCTGTCCCTG	TCACCGGGGG	CCCTGTACGT	CTGAGGCCGA	5400
GGGAAAGCTA	TGGGCGCGGT	TTCTTTCAT	TGACCTGTCG	GTCTTATCAG	TTCTCCGGGT	5460
TGTCAAGGGTC	GACCAAGTTGT	TCCCTTGAGG	TCCGGTTCTT	TCGTTATGG	GGTCATTTT	5520
GGGCCACCTC	CCCAGGTATG	ACTTCCAGGC	GTCGTTGCTC	GCCTGTCACT	TTCCCTCCCTG	5580
TCTCTTTAT	GCTGTGATC	TTTTCTATCT	GTCCTATTG	GACCTGGAGA	TAGGTACTGA	5640
CACGCTGTCC	TTTCCCTATT	AAACACTAAAG	GACACTATAA	AGAGACCCCT	TCGATTTAAG	5700
GCTGTTTGC	TTGTCAGGCC	TATTCTTTT	ACTGGCTTGG	GTCTGTGCG	GTGCTGAAG	5760
CTGTCACCGA	GCCACGCTTC	CTGCTTCCC	GGGCTTGTG	CTTGCCTGTG	CTTGCCTGTG	5820
GCAGCTTGTG	ACAACGGGC	GCTGTACTT	TGCTGGCTG	CAGACCTTT	TCCCGATTTC	5880
CCCGAGGGTGT	CGTGTACAC	CCTGTCCCGG	TGGAATGGT	GGAGCCAGCT	GTGGTTGAGG	5940
GCCACCTTAT	TTCCGCTCAC	TTTTTTTTT	TTTTTTTCTC	TTGGAGTCCTC	GAACCTCCGC	6000
TCTTTTCTCT	TCCCGTCTT	TCTTCCACAT	GCCTCCCGAG	TGCATTTCTT	TTTGTTTTT	6060
TTCTTTTTT	TTTTTTTTT	TTGGGGAGGT	GGAGAGTCCTC	GAGTACTTCA	CTCCTGTCTG	6120
TGGGTCTCAA	GTGTTCATGC	CACGTGCC	CCGAGTGCAC	TTTTTTTTGT	GGCAGTCGCT	6180
CGTTGTGTT	TCTTGTCTG	TGTCTGCCG	TATCAGTAAC	TGTCTGCCC	CGCGTGTAA	6240
ACATTCCAT	CTCGCTTGT	TCTCCGATT	GGCGTGTGTT	GCTCACTCTT	AGATCGATGT	6300
GGTGCTCCGG	AGTTCTCTTC	GGGCCAGGGC	CAAGCCGCGC	CAGGCCAGGG	ACGGACATT	6360
ATGGCGAATG	GCGGCCGCTC	TTCTCGTCT	GGCAGCGGGC	CCCTGCTCT	CCACCCCCATC	6420
CGTGTGCCGG	TGGTGTGGT	AAGGCAGGGG	TGCGGCTCTC	CGGCCCGACG	CTGCCCGCG	6480
CGCACCTTTC	TCAGTGGTTC	CGCGTGGCTC	TGCGGATGTG	TGAGGCCGCCC	GGTTGTGCC	6540
TCACGTGTTT	CACTTGGTC	TGTCCTGCT	TGACCATGTT	CCCAGAGTCG	GTGGATGTGG	6600
CCGGTGGCGT	TGACATACCC	TCCCCTGCTG	TGTCGTGACG	CGCTGTTCT	TGAAAGCGTC	6660
GAGGTGCTCC	TGGAGCGTTC	CAGGTTGTC	TCCTAGGTGC	CTGCTCTGA	GCTGGTGGTG	6720
GCGCTCCCCA	TTCCCTGGTG	TGCCTCCGGT	GCTCCGTCTG	GCTGTGTGCC	TTCCCGTTTG	6780
TGTCTGAGAA	GCCCCGTGAGA	GGGGGGTCGA	GGAGAGAAGG	AGGGGCAAGA	CCCCCCTTCT	6840
TCGTCGGGTG	AGGCGCCAC	CCCAGCACTA	GTACGCCTGT	GCGTAGGGCT	GGTGCTGAGC	6900
GGTCGCGCT	GGGGTTGGAA	AGTTTCTCGA	GAGACTCAT	GCTTCCCCGT	GGGGAGCTTT	6960
GAGAGGCCG	GCTTTCGGGG	GGGACCGGTT	GCAGGGCTC	CCCTGTCGCC	GGATGCTCAG	7020
AATGCCCTG	GAAGAGAAC	TTCTGTTG	CGCAGACCCC	CCCGCGCGGT	CGCCCGCGGT	7080
TTGGTCTTCT	GGTTTCCCTG	TGTGCTGTC	GCATGCATCC	TCTCTCGGTG	GCCGGGGCTC	7140
GTCGGGGTTT	TGGGTCCGTC	CCGCCCTCAG	TGAGAAAGTT	TCCTTCTCTA	GCTATCTTCC	7200
GGAAAGGGTG	CGGGCTTCTT	ACGGTCTCGA	GGGGTCTCTC	CCGAATGGTC	CCCTGGAGGG	7260
CTCGCCCCCT	GACCGCTCC	CGCGCGCGCA	GGCTTGTCTC	TCTCGTCTAC	CGCGGCCCGC	7320
GGCCTCCCCG	CTCCGAGTT	GGGGAGGGAT	CACGCGGGGC	AGAGCCTGTC	TGTCGTCTG	7380
CCGTTGCTGC	GGAGCATGTG	GCTCGGTTG	TGTCGGTTGGT	GGCTGGGAG	AGGGCTCCGT	7440
GCACACCCCC	GCGTGCCTCG	ACTTTCTCC	CTCTCTGAGG	GCCGCGCTGC	GGACGGGGTG	7500
TGGGTAGCG	ACGGTGGCT	CCCGGGTCCC	CACCGTCTC	CCCGTGCCTC	ACCCGTGCCT	7560
TCCGTCGCGT	GCGTCCCTCT	CGCTCGCGT	CGACGACTT	GGCCGCTCCC	CGACGGCGGC	7620
CTGCGCCCG	CGTGGTGCCT	GCTGTGTGCT	TCTCGGGCTG	TGTGGTTGTG	TCGCCTCGCC	7680
CCCCCTTCC	CGCGGCAGCG	TTCCCCACGGC	TGGCGAAATC	GCGGGAGTC	TCCTTCCCC	7740
CCTCGGGGTC	GAGAGGGTCC	GTGTCTGGCG	TTGATTGATC	TCGCTCTCGG	GGACGGGACC	7800
GTTCTGTGGG	AGAACGGCTG	TTGGCCCGT	CCGGCGCGAC	GTCGGACGTG	GGGACCCACT	7860
GCCGCTCGGG	GGTCTTCGTC	GGTAGGCATC	GGTGTGTGCG	CATCGGTCTC	TCTCTCGTGT	7920
CGGTGTGCC	TCCTCGGGCT	CCCGGGGG	CGTCGTGTTT	CGGGTCGGCT	CGGGCGCTGCA	7980
GGTGTGGTGG	GACTGCTCAG	GGGAGTGGTG	CAGTGTGATT	CCCGCCGGTT	TTGCCTCGCG	8040
TGCCCTGACC	GGTCCGACGC	CCGAGCGGTC	TCTCGGTCCC	TTGTGAGGAC	CCCCCTCCGG	8100
GAGGGGCCG	TTTCGGCCGC	CCTTGCCGTC	GTGCGGCCG	CTCGTTCTGC	TGTGTGTTTC	8160
CCCCCTCCCC	GCTCGCCGCA	GCCGGTCTT	TTTCCTCTCT	CCCCCCCC	CCTCTGACTG	8220
ACCCGTGGCC	GTGCTGTCGG	ACCCCCCGCA	TGGGGGCCGCG	CGGGCACGTA	CGCGTCCGGG	8280
CGGTCAACCGG	GGTCTTGGGG	GGGGGCCGAG	GGGTAAGAAA	GTCGGCTCGG	CGGGCGGGAG	8340
GAGCTGTGGT	TTGGAGGGCG	TCCCCGGCCCC	GGGGCCGTGG	CGGTGTCTTG	CGCGGTCTTG	8400

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GAGAGGGCTG	CGTGCAGGG	GAAAAGTTG	CCCCGCGAGG	GCAAAGGGAA	AGAGGCTAGC	8460
AGTGGTCATT	GTCCCACGG	TGTGGTGGTC	TGTTGGCCGA	GGTGCCTCTG	GGGGGCTCGT	8520
CCGGCCCTGT	CGTCCGTCGG	GAAGGCGCGT	GTGCCCCGCT	GCGGAGTGC	CGAGGTGGGT	8580
ACCCTGGCGG	TGGGATTAAC	CCCGCGCGC	TGTCCTCGTG	TGGCGTGGG	GGCTCCGGTC	8640
GATGTCTACC	TCCCTCTCCC	CGAGGTCTCA	GGCCTTCTCC	GCGGGGCTC	TCGGCCCTCC	8700
CCTCGTTCTC	CCCTCTCGCG	GGGTTCAAGT	CGCTCGTCGA	CCTCCCTCTC	TCCGTCTTC	8760
CATCTCTCGC	GCAATGGCGC	CGCCCGAGTT	CACGGTGGGT	TCGTCCTCCG	CCTCCGCTTC	8820
TCGCCGGGG	CTGGCGCTG	TCCGGTCTCT	CCTGCCGAC	CCCCGTTGGC	GTGGTCTTCT	8880
CTCGCCGGG	TCGCGGACTC	CTGGCTTCGC	CCGGAGGGTC	AGGGGGCTTC	CCGGTCTCCCC	8940
GACGTTGCGC	CTCGCTGCTG	TGTGCTTGGG	GGGGGCCCGC	TGCGGCCCTCC	GCCC GCCCGT	9000
GAGCCCCTGC	CGCACCCGCC	GGTGTGGGGT	TTCGCGCCGC	GGTCAGTTGG	GCCCTGGCGT	9060
TGTGTGCGGT	CGGGAGCGTG	TCCGCCTCGC	GGCGGCTAGA	CGCGGGTGTG	GCCGGGCTCC	9120
GACGGGTGGC	CTATCCAGGG	CTCGCCCCCG	CCGACCCCCCG	CCTGCCCGTC	CCGGTGGTGG	9180
TCGTTGGTGT	GGGGAGTGA	TGGTGTCTACC	GGTCATTCCC	TCCC CGCGTGG	TTTGA CTC	9240
TCGCCGGTGT	CGCGCTTCTC	TTTCCGCCAA	CCCCCACGCC	AACCCACAC	CCTGCTCTCC	9300
CGGGCCGGTG	CGGTGACGCT	TCCGGCTCTC	CCGATGCCGA	GGGGTCTCGGG	ATT TGTGCCG	9360
GGGACGGAGG	GGAGAGCGGG	TAAGAGAGT	GTGCGAGAGC	TGTCCCGGGG	CGACGCTCGG	9420
GTTGGCTTTG	CCCGCGTGC	GTGCTCGCGG	ACGGGTTTTTG	TCGGACCCCCG	ACGGGGTCGG	9480
TCCGGCCGCA	TGCACTCTCC	CGTTCCGCGC	GAGCGCCCGC	CCGGCTCAC	CCC GTTTGT	9540
CCTCCCGCGA	GGCTCTCCGC	CGCCGCCGCC	TCCTCCCTCC	CTCTCGCGT	CTCTGTCCCC	9600
CCTGGTCTCG	TCCCACCCCC	GACGCTCCGC	TCGCGCTTCC	TTACCTGGTT	GATCCTGCCA	9660
GGTAGCATAT	GCTTGTCTCA	AAGATTAAGC	CATGCATGTC	TAAGTACGCA	CGGCCGGTAC	9720
AGTGA AACTG	CGAATGGCTC	ATTAAATCAG	TTATGGTTCC	TTTGGTCGCT	CGCTCCTCTC	9780
CTACTTGGAT	AACTGTGGTA	ATTCTAGAGC	TAATACATGC	CGACGGGCCG	TGACCCCCCT	9840
TCCC GGGGGG	GGATGCGTC	ATTATACAGA	TCAAAACCAA	CCCGGTGAGC	TCCCTCCCCG	9900
CTCCGGCCCG	GGGTGCGGGC	CCGGCGCTT	GGTGACTCTA	GATAAACCTCG	GGCCGATCGC	9960
ACGCCCCCG	TGGCGGCGAC	GACCCATTG	AACGTCTGCG	CTATCAACTT	TCGATGGTAG	10020
TCGCCGTGCC	TACCATGGTG	ACCACGGGT	ACGGGGAAATC	AGGGTTCGAT	TCCGGAGAGG	10080
GAGCCTGAGA	AACGGCTACC	ACATCCAAGG	AAGGCAGCAG	GCGCGCAAAT	TACCCACTCC	10140
CGACCCGGGG	AGGTAGTGA	GAAAAATAAC	AATACAGGAC	TCTTCGAGG	CCCTGTAAATT	10200
GGAATGAGTC	CACTTTAAAT	CCTTAACGA	GGATCCATTG	GAGGGCAAGT	CTGGTGCCAG	10260
CAGCCGCGGT	AATTCCAGCT	CCAATAGCGT	ATATTAAAGT	TGCTGCAGTT	AAAAAGCTCG	10320
TAGTTGGATC	TTGGGAGCGG	GCGGGCGGT	CGCCGCGAGG	CGAGTCACCG	CCCGTCCCCG	10380
CCCCTTGCC	CTCGCGGCC	CCTCGATGCT	CTTAGCTGAG	TGTCCTCGGG	GGCCCGAAGC	10440
GTTTACTTG	AAAAAATAG	AGTGTCAAA	GCAGGCCCCG	GCCGCGCTGG	TACCGCAGCT	10500
AGGAATAATG	GAATAGGACC	GCGGGTTAT	TTTGTGGTT	TTCGGA ACTG	AGGCCATGAT	10560
TAAGAGGGAC	GGCCGGGGGC	ATTCTGATTG	CGCCGCTAGA	GGTGA AATT	TTGGACCGGC	10620
GCAAGACGGA	CCAGAGCGAA	AGCATTGCG	AAGAATGTT	TCATTAATCA	AGAACGAAAG	10680
TCGGAGGTT	GAAGACGATC	AGATACCGTC	GTAGTCCGA	CCATAAACGA	TGCCGACTGG	10740
CGATGCGGG	CGCGTATTCC	CATGACCGC	CGGGCAGCTT	CCGGGAAACC	AAAGTCTTTG	10800
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CCAGGAGTGG	GCCTCGGGCT	TAATTTGACT	CAACACGGGA	AACCTCACCC	GGCCCGGACA	10920
CGGACAGGAT	TGACAGATTG	ATAGCTCTT	CTCGATTCTG	TGGGTGGTGG	TGCATGGCCG	10980
TTCTTAGTTG	GTGGAGCGAT	TTGCTCGGT	AATTCCGATA	ACGAACGAGA	CTCTGGCATG	11040
CTAATAGTT	ACGGCACCCC	CGAGCGCTCG	CGCTCCCCCA	ACTTCTTAGA	GGGACAAGTG	11100
CGCTTCA GGC	ACCCGAGATT	GAGCAATAAC	AGGTCTGTGA	TGCCCCCTAGA	TGTCCGGGGC	11160
TGCA CGCGCG	CTACACTGAC	TGGCTCAGCG	TGTGCCCTACC	CTGCGCCGGC	AGGCGCGGGT	11220
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GAATTCCCAG	TAAGTGCAGG	TCATAAGCTT	GGCTTGTATTA	AGTCCCTGCC	CTTTGTACAC	11340
ACCGCCCCGTC	GCTACTACCG	ATTGGATGGT	TTAGTGA GGC	CCTCGGATCG	GCCCCGCCGG	11400
GGTCGGCCCA	CGGGCCCTGGC	GGAGCGCTGA	GAAGACGGTC	GAAC TTGACT	ATCTAGAGGA	11460
AGTAAAAGTC	GTAACAAGGT	TTCCGTAGGT	GAACCTCGC	AAGGATCATT	AAACGGGAGA	11520
CTGTGGAGGA	CGCGCGCGGT	GGCCCCTCT	CCCCGCTT	TGTGTGTCCT	CGCCGGGAGG	11580
CGCGTGC	CGGGGCTCCG	TGCGCCCGT	GTGGAGCGAG	GTGTCTGGAG	TGAGGTGAGA	11640
GAAGGGGTGG	GTGGGGTCCG	TCTGGTCCG	TCTGGGACCG	CCTCCGATTT	CCCCTCCCCC	11700
TCCCCTCTCC	CTCGTCCGGC	TCTGACCTCG	CCACCCCTACC	GCGGGGGCGG	CTGCTCGCGG	11760
CGCTTCTGCC	TCTTCTCCGT	CCGGCTCTTC	CGTGTCTACG	AGGGGCGGTA	CGTCGTTACG	11820
GGTTTTGAC	CCGTCCTCGG	GGCGTTCGGT	CGTCTGGGGC	CGCGCTTTGC	TCTCCCGGCA	11880
CCCATCCCCG	CCGCGGCTCT	GGCTTTCTA	CGTTGGCTGG	GGCGGGTTGTC	GCGTGTGGGG	11940
GGATGTGAGT	GTCGCGTGTG	GGCTCGCCCG	TCCCAGATGCC	ACGCTTTCT	GGCCTCGCGT	12000
GTCCTCCCCG	CTCCGTCTCC	GGGTACCTAG	CTGTCGCGT	CCGGCGCGGA	GGTTTAAGGA	12060
CCCCGGGGGG	GTGCCCTCTG	CGCCCCCAGG	GTCGGGGGGC	GGTGGGGCCC	GTAGGGAAAGT	12120
CGGTGTTCG	GGCGGGCTCTC	CCTCAGACTC	CATGACCCCTC	CTCCCCCCGC	TGCGGCCGTT	12180
CCCGAGGCGG	CGGTGCGTGTG	GGGGGGTGG	TGTCCTGGAGC	CCCCTCGGGC	GCCGTGGGGG	12240
CCCGACCCGC	GCCGCCGGCT	TGCCCCGATT	CCGCGGGTGC	GTCCTGTCGG	TGCGGGTCGT	12300
GGGTTCCCGT	GTCGTTCCCG	TGTTTTTCCG	CTCCCGACCC	TTTTTTTTTC	CTCCCCCCCCA	12360
CACGTGTC	GTTTCGTTCC	TGCTGGCGG	CCTGAGGCTA	CCCCTCGGGC	CATCTGTTCT	12420

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CCTCTCTCTC	CGGGGAGAGG	AGGGCGGTGG	TCGTTGGGGG	ACTGTGCCGT	CGTCAGCACC	12480
CGTGAGTCG	CTCACACCCG	AAATACCGAT	ACGACTCTTA	GCGGTGGATC	ACTCGGCTCG	12540
TGCGTCGATG	AAGAACGCAG	CTAGCTCGA	GAATTAAATGT	GAATTGCGAGG	ACACATTGAT	12600
CATCGACACT	TCGAACGCAC	TTGCGGCCCC	GGGTTCCCTC	CGGGGCTACG	CCTGTCTGAG	12660
CGTCGGTTGA	CGATCAATCG	CGTCACCCGC	TGCGGTGGGT	GCTGCGCAGG	TGGGAGTTTG	12720
CTCGCAGGGC	CAACCCCCCA	ACCCGGTGC	GGCCCTCCGT	CTCCCGAAGT	TCAGACGTGT	12780
GGGGCGGTGT	CGGTGTGGCG	CGCGCGCCCG	CGTCCGGGAG	CCTGGTCTCC	CCC CGC CATC	12840
CGCGCTCGCG	GCTTCTTCCC	GCTCGCCGT	TCCC GCCCTC	GCCC GTGCAC	CCC CGT CCGT	12900
GCCTCGCGTC	GGCGCCTCCC	GGACCGCTGC	CTCACCAAGTC	TTTCTCGGT	CCGT GCG CCC	12960
TGGGAACCCA	CCCGCGCCCC	GTGGCGCCCG	GGGGTGGGGG	CGTCCGCATC	TGCTCTGGTC	13020
GAGGTTGGCG	GTTGAGGGTG	TGCGTGCGCC	GAGGTGGTGG	TCGGTCCCCT	GCGGCCGCGG	13080
GGTTGTCGGG	GTGGCGGTG	ACGAGGCCG	GTCGGTGC	TGCGGTGGTT	GTCTGTGTGT	13140
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GTATCCCCGG	TGGCGTTGCG	AGGGAGGGT	TGCGTGC	CGTCCGTCCG	TCCCTCCCTC	13320
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CCCGGGGAGC	CCCGCGCGTC	CGTGCGCCGA	TGCGAGTCAC	CCCCGGGTGT	TGCGAGTTG	13500
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TGTCCCCCCT	TTCTGACCGC	GACCTCAGAT	CAGACGTG	GACCCGCTGA	ATTAAAGCAT	13800
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GAAGAGCCCA	GGCGCGAAC	CCC CGCGC	GTGCGCGCGT	GGGAATATGT	CGCTACGGAA	13920
GACCCACTC	CCGGCGCCGC	TCTGGGGGG	CCCAAGGCT	TCTGATCGAG	GCCCAGCCCC	13980
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CGAGACCGAT	AGTCAACAAG	TACCGTAAGG	GAAAGTTGAA	AAGAACCTTG	AAGAGAGAGT	14160
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CGGACTGTCC	CCAGTGC	CCGGGCGTC	TCGCGCCGTC	GGGTCCC	GGGACCGTCG	14820
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TGTGATTCT	GCCCCAGTGT	CTGAATGT	AAGTGAAGA	ATTCAATG	GCGCGGGTAA	17160
ACGGCGGGAG	TAACTATGAC	TCTCTTA	AGG TAGCCAAT	CCTCGTC	TAATTAGTGA	17220
CGCGCATGAA	TGGATGAACG	AGATTCCC	AGTCCCTAC	TACTATCC	CGAAACACAA	17280
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GCCCCGTCT	CGCGTCGGG	TCGGGGC	CCGGCTC	GGGCGCC	TGAAATACCA	17460
CTACTCTCAT	CGTTTTTCA	CTGACCC	GAGGCGGGG	GGCGAGCCC	GAGGGGCTCT	17520
CGCTTCTGGC	GCCAAGCGTC	CGTCCC	GTGCGGGCG	GC	CTCGGGGAC	17580
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ATCTTGATTT	TCAGTACGAA	TACAGAC	GAAAGCGGG	CCTCACG	CTTCTGACCT	17760
TTTGGGTTT	AAGCAGGAGG	TGTC	CAGAAA GTTAC	GGATAACTG	CTTGTGGCGG	17820
CCAAGCGTC	ATAGCGACGT	CGCTT	TCCTTCGAT	TCGGCTCTC	CTATCATTGT	17880
GAAGCAGAA	TCACCAAGCG	TTGGATG	CACCC	TAGGGAAC	GAGCTGGGTT	17940
TAGACCGTC	TGAGACAGGT	TAGTTT	TAC	TGTGTGTT	CCATGGTAAT	18000
CCTGCTCAGT	ACGAGAGGAA	CCGCAGG	AGACATTG	TGTATG	TGGCTGAGGA	18060
GCCAATGGGG	CGAACGCTACC	ATCTG	TTATGACTG	ACGCCTCTAA	GTCAGAATCC	18120
GCCCAAGCGG	AACGATAACGG	CAGCGC	GGAGCCTCG	TTGGCCCGG	ATAGCGGGT	18180
CCCCGTCCGT	CCCGCTCGGC	GGGGT	CGTCGCCCC	CGCGCGCG	GGGTCTCCC	18240
CCGCCGGGGC	TCGGGACCGG	GGTCCGGT	GGAGAGCCG	TCGTCTTGG	AAACGGGGT	18300
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GACCAGATAT	CCGAAAGTC	TCTCTT	TTTACT	CCCACAGC	TTCTCTTT	19380
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CCGCGACGCG	GGGGCTTCAC	TCTGG	ACTCT	TTTTTTT	TTAAATTTC	19620
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ATTGAACTC	AGGACCCTGG	CAGGTCAACT	GGAAAACGTG	TTTCTATAT	ATATAAATAG	20640
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TGCTTTTTT	TTCTCTCTGA	GACAGTATT	CTCTGTGTA	CCTGGTGC	TGAAACTCAC	20760
TCTGTAGACC	AGCCTGGCT	CAATCGAAC	CGAAAATCC	CCTGCCTCT	GTCTACCTCC	20820
CAATTGGA	GTAAAGGTGT	GCTACACAC	TGCGCTGGCAT	TATTATCATT	ATCATTATTA	20880
ATTTTATTAT	TAGACAGAAC	GAAATCAACT	AGTTGGTCCT	GTTTCGTTAA	TTCATTGAA	20940
ATTAGTTGGA	CCAATTAGTT	GGCTGGTTG	GGAGGTTCT	TTTGTTC	ATTTGGGTGT	21000
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CCAGTTCCCTC	CTGCCTCTG	GAAGATGTAG	GCATTGCATT	GGGAAAAGCA	TTGTTTGAGA	21240
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TGTTCTCACT	CTGCCACCAA	CGCGCTTGT	ACATTGAATG	TGAGCTTTGT	TTTGCTTAAC	21420
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TTCCCAAGACG	GCCTTTGAG	AATAAAATGG	GAGGCCAGAA	CCAAAGTCTT	TTGAATAAAG	21540
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TGAATGATCC	CAGCATGGG	AGACAGTCTG	CCCTCTTGT	GGTATATCAC	CATATACTCA	21840
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TACCTGAAGT	CCCTGAGTGA	TGATTTCCCT	GTGAATT			22118

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42999 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCTGACACGC	TGTCCCTCTGG	CGACCTGTG	TCGGAGAGGT	TGGGCCTCCG	GATGCGCGCG	60
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GGGTCCGGGT	CTCTGACCCA	CCCAGGGCG	GGGGGGAAAGG	CGCGAGGGC	CACCGTGGCC	240
CGTGCCTCT	CCGCTGCGGG	CGCCCCGGGC	GCCGACAAAC	CCCACCCGCT	GGCTCCGTGC	300
CGTGCCTGTC	AGGCCTTCTC	GTCTCCGCGG	GGTTGTC	CGCCCTTCTCC	CCGGAGTGGG	360
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ATCGATGTGG	TGACGTCGTG	CTCTCCCGG	CCGGGTCCGA	GCCGCGACGG	GCGAGGGCG	480
GACGTTCTG	CGCAACGGGA	CCGTCCTCT	CGCTCCGCC	GCGCGGTCCC	CTCGTCTGCT	540
CCTCTCCCCG	CCCCCGGGCC	GGCGTGTGGG	AAGGCGTGGG	GTGCGGACCC	CGGCCCGAAC	600
TCGCCGTCCC	CCCCCGCCGCC	TTCGCTCGC	GGGTGCGGGC	CGGCGGGGTC	CTCTGACCG	660
GCAGACAGCC	CTGCCGTGCG	CCTCCAGTGG	TTGTCGACTT	GCGGGCGGCC	CCCCTCCCG	720
CGGGTGGGGG	TGCCGTCCCG	CCGGCCCGTC	GTGCTGCCCT	CTCGGGGGGG	TTTGCGCGA	780
CGCTCGGCC	CGCCTGGGCC	CTTGCCTGTC	TCTCTGGAGCG	CTCCGGGTTG	TCCCTCAGGT	840
GCCCGAGGCC	GAACGGTGGT	GTGTCGTTCC	CGCCCCCGGC	GCCCCCTCCT	CCGGTCGCCG	900
CCGCGGTGTC	CGGCCGTGGG	TCCGTAGGGG	GCTCGTCTGG	GTGGGGTTTCG	AGGGGGTTTG	960
AGTGAGACGA	GACCGAGACG	GCCCCCTCCCA	CGCGGGGAAG	GGCAGCCGCC	TGCTCTCGGT	1020
GAGCGCACGT	CCCGTGTCTC	CCTCTGGCGG	GTGCGCGC	GCCGTGTGAG	CGATCGCGGT	1080
GGGTTCGGGC	CGGTGTGACG	CGTGCCTGCC	CCGGCCGCC	AGGGGCTGCC	GTTCTGCC	1140
CGACCGGTG	TGTGTGGGTT	GACTTCGGAG	GCGCTCTGCC	TCGGAAGGAA	GGAGGTGGGT	1200
GGACGGGGGG	GCCTGGTGGG	GTTGCGCGCA	CGCGCGCAC	GGCCGGGCC	CCGCCCTGAA	1260
CGCGAACGCT	CGAGGTGGCC	CGCGCAGGT	GTTTCTCGT	ACCGCAGGGC	CCCCTCCCTT	1320

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Cont

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GTACCGGATC	CCCCGGGCCG	CCGCCTCTGT	CTCTGCCTCC	TTTATGGTAG	CGCTGCCGTA	1500
GCGACCCGCT	CGCAGAGGAC	CCTCCTCCGC	TTCCCCCTCG	ACGGGGTTGG	GGGGGAGAAG	1560
CGAGGGTCC	GCCGGCCACC	GCGGTGGTGG	CCGAGTGCAG	CTCGTCGCCT	ACTGTGGCCC	1620
GCGCCTCCCC	CTTCGGAGTC	GGGGGAGGAT	CCCGCCGGGC	CGGGCCCGGC	GCTCCCACCC	1680
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CGCGTACCC	CCTCGTCCG	CGAGTCGCT	CTTCGGCCCG	TCCCGTGCCT	AGTCGTGACC	1800
GGTGCCGACG	ACCGCGTTTG	CGTGGCACGG	GGTCGGGCC	GCCTGGCCCT	GGAAAGCGT	1860
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CCCCGCGCTG	GACCGAACCC	GGCACCGCCT	CGTGGGGCGC	CGCCGCCCGG	CACTGATCGG	2340
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CCGCGCGTGT	GTCCCGGCTG	CGGTCGGCCG	CGCTCGAGGG	GTCCCCGTGG	CGTCCCCTTC	2640
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CGGGCGCTGC	GGGGCCCTTC	CCCGAGGCAG	CGCTCCCGG	CGTCGCGTGC	GGGGAGAGCC	2820
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GGTCCTCCCC	GGACAGGCGT	TCGTGCGACG	TGTGGCGTGG	GTGACACCTCC	GCCTTGCCGG	2940
TCGCTCGCCC	TCTCCCGGGG	TCGGGGGGTG	GGGCCCCGGG	CGGGGCCCTG	GGCCCGGTGCG	3000
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GCTGTGCTGT	ACTGTCGTG	ATCCCAGCTA	CTCGGGAGGC	CGAGCTGAGG	CAGGAGAAC	38940
GCTTGAAACT	GGGAGGCGGA	GGTTGCAAGT	AGCCGAGATC	GCGCCACTGC	AACCCAGCCT	39000
GGGCGACAGA	GCGAGACTCC	GTCTCCAAA	AATGAAAATG	AAAATGAAAC	GCAACAAAAT	39060
AATTAAAAAG	TGAGTTCTG	GGGAAAAAGA	AGAAAAGAAA	AAAGAAAAAA	ACAACAAAAC	39120
AGAACAAACCC	CACCGTGACA	TACACGTACG	CTTCTCGCCT	TCGAGGGCCT	CAAACACGTT	39180
AGGAATTATG	CGTGATTTCT	TTTTTAAC	TCATTTTATG	TTATTATCAT	GATTGATGTT	39240
TCGAGACGGA	GTCTCGGAGG	CCCGCCCTCC	CTGGTTGCC	AGACAACCCC	GGGAGACAGA	39300
CCCTGGCTGG	GCCCGATTGT	TCTTCTCCTT	GGTCAGGGGT	TTCCCTGTCT	TTCTTCGTGT	39360
CTTAAACCCG	CGTGGACTCT	TCCGCCTCGG	TTGTCAGACAGA	TGGCAGCTCC	ACTTTAGGCC	39420
TTGTTGTTGT	TGGGGACTTT	CCTGATTC	CCCAGATGTA	GTGAAAGCAG	GTAGATTGCC	39480
TTGCCTGGCC	TTGCGCTGGCC	TTGCCTTTTC	TTCTCTTCTT	TCTTCTTTTA	TTACTTTCTC	39540
TTTTCTTCT	TCTTCTTCTT	CTTTTTTTG	AGACAGAGTT	TCACTCTTGT	TGCCCAGGCT	39600
AGAGGGCAAT	GGGCGATCT	CGGCTCACCG	CACCCCTCCGC	CTCCCAGGTT	CAAGCGATTC	39660
TCCTGCCTCA	GCCTCCTGAT	TAGCTGGAT	TACAGGCATG	GGCCACCGTG	CTGGCTGATG	39720
TTTGTACTTT	TAGTAGAGAC	GGTGTTTTTC	CATGTTGGTC	AGGCTGGTCT	CCCACTCCCA	39780
ACCTCAGGTG	GTCCGCTCGC	CTTAGCTCC	CAAAGTGTG	GGATGACAGG	CGTGCAACCG	39840
CGCCCCAGCCT	CTCTCTCTCT	CTCGCTCGT	TGCTGCTTG	CTTTCGTGT	39900	
TTCTTGCTTT	CCCGTTTTCT	TGCTTCTTCTT	TTTCTTCTCAT	GCTTGCTTTC	39960	
TTGCTTGCTT	GCTTGTCTTC	GTGCTTCTTCT	GCTTCTCTGT	TTTCTTCTTCT	40020	
TTTCTTCTTCT	TTGTTTCTTT	CTTGCTGCT	TTCTTGCTTG	CTTGCTTGCT	TTCTGTGCTT	40080
CTTGCTTCTC	TGTTTCTTT	CTTCTTTCT	TTCTTTCTTCT	TCTTTCTTGC	TTGCTTTCTC	40140
GCTTGCTTGC	TTTCGTGCTT	TCTTGTTTCT	TCGATTTCTT	TCTTTCTTTT	GTTCCTTCTC	40200
TGCTTGCTTT	CTTGCTTGCT	TGCTTCTCGT	CTTCTTGCTT	TCCTGTTTTC	TTTCTTCTTT	40260
TCTTCTTCTT	GTTTCTTCTT	TGCTTCTGTT	CTTGCTTGCT	TGCTTCTGTT	CTGTTCTGTT	40320
TCTCGATTTG	TTTCTTCTT	TTGTTTCTT	CTTGCTTGCT	TTCTTGCTTG	ATTGCTTTCG	40380
TGCTTCTTCTG	CTTCTTCTGTT	TTCTTCTT	CTTTGTTTCT	TTCTTCTTCT	GCTTCCTTGT	40440
TTTCTTGCTT	TCTTGTCTGC	TTGCTTCTG	GCTTCTTCTGT	TTTCTTGCTT	TCTTTCTTTT	40500
GTTTCTTCT	TGCTTGTCTT	CTTGCTTCT	TGTTTCTTCTG	CTTTCTTGCT	TGCTTGCTTT	40560
CGTGTCTTCT	TTCTTGCTTT	CTTTCTTCT	TTTCTTTCT	TTTCTTCTTCT	TTCTTGCTTT	40620
CTTTCTTCTC	ATCATCATCT	TTCTTCTT	CTTTCTTCTC	TTTCTTCTTCT	TCTATCTTC	40680
TTTCTTCTTCT	TCTTCTTCTC	TTTCTTCT	TCTTCTGTT	TCGTCTTTT	GAGACAGAGT	40740
TTCACTCTTG	TTTCCACGGC	TAGAGTGAA	TGGCGCGATC	TTGGCTCAC	GCACCTTCCG	40800
CCTCCCGGGGT	TCGAGCGCTT	CTCCTGCCTC	CAGCCTCCCG	ATTAGGGGG	ATTGACAGGG	40860
AGGCACCCCC	ACGGCTGGCT	TGGCTGATGT	TTGTGTGTTT	AGTAGGCACG	CCGTGCTCT	40920
CCATGTTGCT	CAGGCTGGTC	TCCAACTCCC	GACCTCTGT	GATGCGCCCA	CCTCGGCCCTC	40980
TCGAAGTGCT	GGGATGACGG	CGCTGACGAC	CGTGGCCGGC	CTGTTGACTC	ATTCGCTTT	41040
TTTATTTCTT	TCGTTTCCAC	GCGTTTACTT	ATATGTATTA	ATGAAACGT	TTCTGTACGC	41100
TTATATGCAA	ACAAACGACAA	CGTGTATCTC	TGCATTGAAT	ACTCTGCGT	ATGGTAAATA	41160
CGTATCGGTT	GTATGGAAAT	AGACTTCTGT	ATGATAGATG	TAGGTGCTG	TGTTATACAA	41220
ATAAAATACAC	ATCGCTCTAT	AAAGAAGGGA	TCGTCGATAA	AGACGTTTAT	TTTACGTATG	41280
AAAAGCGTCG	TATTATGTG	TGTAATGAA	CCGAGCGTAC	GTAGTTATCT	CTGTTTTCTT	41340
TCTCTCTCTC	CTTCGTGTTT	TTCTTCTCTC	CTTTCTGCTC	TTTTTCTCTT	CGTGTCTTAT	41400
TTCTTCTCT	CTTCCTTTCC	TTCTTCTCT	CTTTCTGCTC	TTTTTCTCTT	TTCTGTGTTT	41460
TTCTCTTTG	TTCCCTGTGT	TTCTTCTCTT	TTTCTTCTCT	CTCTGTTCT	TTTCCCTTTC	41520

TTTCCCTTCGT	TTCTTTCCCTC	ATTCTTTCTC	TCTTTTCGTT	TGTTTCTTTC	CTTCCCGTCT	41580
GTCTTTTAAA	AAATTGGAGT	GTTTCAGAAG	TTTACTTTGT	GTATCTACGT	TTTCTAAATT	41640
GTCTCTCTT	TCTCCATTTC	CTTCCTCCCT	CCCTCCCTCC	CTCCCTGCTC	CCTTCCCTCC	41700
CTCCCTCCCT	TTCGCCCATCT	GTCTCTTTTC	CCCACCTCCCC	TCCCCCCGTC	TGTCTCTGCG	41760
TGGATTCCGG	AAGAGCCTAC	CGATTCTGCC	TCTCCGTGTG	TCTCGAGCGA	CCCCGCGACC	41820
GAGTCCTTGT	GTGTTCTTTC	TCCCTCCCTC	CCTCCCTCCC	TCCATCTGCC	CCTCCCTGCT	41880
TCCGAGAGGC	ATCTCCAGAG	ACCGCCCGT	GGGTTGTCTT	CTGACTCTGT	CCGGGTGAG	41940
GCAGAGACGC	GTGTTGGGCA	CCGTTTGGT	GGGGTTGGGG	CAGAGGGGCT	CGGTTTCGG	42000
CCTCGGGAAAG	AGCTTCTCGA	CTCACGGTT	CGCTTTCGCG	GTCCACGGGC	CGCCCTGCCA	42060
GCCGGATCTG	TCTCGCTGAC	GTCCGCCGGC	GTGTCGGGC	TCCATCTGGC	GGCGCGTTG	42120
AGATCGTGT	CTCGGCTTCC	GGAGCTGCC	TGGCAGCTGC	CGAGGGAGGG	GACCGTCCCC	42180
GCTGTGAGCT	AGGCAGAGCT	CCGGAAAGCC	CGCGGTGCTC	AGCCCCGGCTG	GCCCCTGGC	42240
GCCAGAGCTG	TGGCCGGTCG	CTTGTGAGTC	ACAGCTCTGG	CGTGCAGGTT	TATGTGGGG	42300
AGAGGCTGTC	GCTGCGCTTC	TGGGCCCGCG	GCGGGCGTGG	GGCTGCCCGG	GCCGGTGCAC	42360
CAGCGCCGGC	TAGCTCCCGA	GGCCCGAGCC	GCGACCCGGC	GGACCCGCCG	CGCGTGGCGG	42420
AGGCTGGGA	CGCCCTTCCC	GGCCCGGTG	CGCTCCCGCT	ATCCTGGCCG	TCTGAGGGCG	42480
CGGCCGAATT	CGTTTCCGAG	ATCCCCGTG	GGAGCCGGGG	ACCGTCCCCTC	CCCCGTCCCC	42540
CGGGTGCCTG	GGAGCGGTCC	CCGGGCCGGG	CCCGGGTCCC	TCTGCCGCA	TCCTTCTGG	42600
CGAGTCCCCG	TGGCCAGTCG	GAGAGCGCTC	CCTGAGCCGG	TGCGGCCGA	GAGGTGCGC	42660
TGGCCGGCCT	TCGGTCCCTC	GTGTGTCCCG	GTCGTAGGAG	GGGCCGGCCG	AAAATGCTTC	42720
CGGCTCCCGC	TCTGGAGACA	CGGGCCGGCC	CCTGCGTGTG	GCCAGGGCGG	CGGGGAGGGC	42780
TCCCCGGCCC	GGCGCTGTCC	CCGCGTGTGT	CCTTGGGTTG	ACCAGAGGGA	CCCCGGGCCG	42840
TCCGTGTGTG	GCTGCGATGG	TGGCGTTTTT	GGGGACAGGT	GTCCGTGTCC	GTGTCGCGC	42900
TCGCCTGGGC	CGGGGGCGTG	GTCGGTGACG	CGACCTCCCG	GCCCCGGGGG	AGGTATATCT	42960
TTCGCTCCGA	GTGGGCAATT	TTGGGCGGCC	GGGTTATAT			42999

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 175 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
  
- (vi) ORIGINAL SOURCE:
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTCCCGCGCG	GCCCCCGTGT	TCGCCGTTCC	CGTGGCGCGG	ACAATGCGGT	TGTGCGTCCA	60
CGTGTGCGTG	TCCGTGCACT	GCCGTTGTGG	AGTGCCTCGC	TCTCCTCCCTC	CTCCCCGGCA	120
CGCTTCCAC	GGTTGGGAC	CACCGGTGAC	CTCGCCCTCT	TCGGGCCTGG	ATCCG	175

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 755 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTCTGGTGG	GAATTGTTGA	CCTCGCTCTC	GGGTGCGGCC	TTTGGGAAAC	GGCGGGGTG	60
GTCGTGCCCG	GCGCCGGACG	TGTGTGGGGG	CCCACTTCCC	GCTCGAGGGT	GGCGGTGGCG	120
GCGGCGTTGG	TAGTCTCCCG	TGTTGCGTCT	TCCCGGGCTC	TTGGGGGGGG	TGCCGTCGTT	180
TTCGGGGCCG	CGCGTTGCTTG	GCTTACGCAG	GCTTGGTTTG	GGACTGCCTC	AGGAGTCGTG	240

GGCGGTGTGA	TTCCCGCCGG	TTTTGCCTCG	CGTCTGCCTG	CTTGCCCTCG	GGTTTGCTTG	300
GTTCGTGTCT	CGGGAGCGGT	GGTTTTTTT	TTTTTCGGGT	CCCAGGGAGA	GGGGTTTTTC	360
CGGGGGACGT	TCCCCTCGCC	CCCTGCCGCC	GGTGGGTTTT	CGTTTCGGC	TGTGTTCGTT	420
TCCCCCTTCCC	CGTTTCGCG	TCGGTTCTCC	CCGGTCGGTC	GGCCCTCTCC	CCGGTCGGTC	480
GCCCCGGCGT	GCTGCCGGAC	CCCCCCCTCT	GGGGGGGATG	CCCGGGCACG	CACGCCTCCG	540
GGCGGCCACT	GTGGTCCGGG	AGCTGCTCGG	CAGGCCGGGTG	AGCCAGTTGG	AGGGGCGTCA	600
TGCCCCCGCG	GGCTCCCCTG	GCCGACGCCG	CGTGTCTTT	GGGGGGGCCT	GTGCCTGCCG	660
GAAGGCTGCG	CACCTTGTCG	GTCCTTGCAG	GGGAAAGAGG	CTTTTTTTT	TTAGGGGGTC	720
GTCCCTCGTC	GTCCCGTCGG	CGGTGGATCC	GGCCT			755

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 463 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCCGAGGTG	CGTCTGCCGG	TTGGGGCTCG	TCCGGCCCCG	TCGTCCCTCCG	GGAAGGCGTT	60
TAGCGGGTAC	CGTCGCCCGC	CCGAGGTGGG	CGCACGTCGG	TGAGATAACC	CCGAGCGTGT	120
TTCTGGTTGT	TGGCGGCCGG	GGCTCCGGTC	GATGTCTTCC	CCTCCCCCTC	TCCCCGAGGC	180
CAGGTCAAGCC	TCCGCCTGTG	GGCTTCGTG	GCCGTCTCCC	CCCCCCTCAC	GTCCCTCGCG	240
AGCGAGCCCG	TCCGTTCGAC	CTTCCTTCCG	CCTTCCCCCC	ATCTTCCGC	GCTCCGTTGG	300
CCCCGGGGTT	TTCACGGCGC	CCCCAACGCT	CCTCCGCCCTC	TCCGCCCGTG	GTTTGGACGC	360
CTGGTTCCGG	TCTCCCGGCC	AAACCCCGGT	TGGGTTGGTC	TCCGGCCCCG	GCTTGCTCTT	420
CGGGTCTCCC	AACCCCGGCC	CGGAAGGGTT	CGGGGGTTCC	GGG		463

*A  
Cont*

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 378 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGATTCTTCA	GGATTGAAAC	CCAAACCGGT	TCAGTTTCCT	TTCCGGCTCC	GGCCGGGGGG	60
GGCGGCCCCG	GGCGGTTGG	TGAGTTAGAT	AACCTCGGGC	CGATCGCACG	CCCCCGTGG	120
CGGCGACGAC	CCATTGAAAC	GTCTGCCCTA	TCAACTTTCG	ATGGTAGTCG	ATGTGCCTAC	180
CATGGTGACC	ACGGGTGACG	GGGAATCAGG	GTTCGATTCC	GGAGAGGGAG	CCTGAGAAC	240
GGCTTACCAACA	TCCAAGGAAG	GCAGCAGGCG	CGCAAATTAC	CCACTCCCGA	CCCGGGGAGG	300
TAGTGACGAA	AAATAACAAT	ACAGGACTCT	TTCGAGGCC	TGTAATTGGA	ATGAGTCCAC	360
TTTAAATCCT	TTAACGAG					378

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 378 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATCCATTGG	AGGGCAAGTC	TGGTGCAGC	AGCCGCGGTA	ATTCCAGCTC	CAATAGCGTA	60
TATTAAAGTT	GCTGCAGTTA	AAAAGCTCGT	AGTTGGATCT	TGGGAGCGGG	CGGGCGGTCC	120
GCCCGCAGGC	GAGTCACCGC	CCGTCCCCGC	CCCTTGCCCTC	TCGGCGCCCC	CTCGATGCTC	180
TTAGCTGAGT	TGTCCCGCGG	GGCCCAGAAC	GTAACTTTG	AAAAAAATTAG	AGTTGTTCA	240
AAGCAGGCC	GAGCCGCCTG	GATAACGCCA	GCTAGGAAAT	AATGGAATAG	GACCGCGGTT	300
CCTATTTGT	TTGGTTTCG	GAACTGAGCC	CATGATTAAG	GGAAACGGCC	GGGGGCATTC	360
CCTTATTGCG	CCCCCTA					378

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGATCTTTC	CGCTCCCCGT	TCCTCCCGGC	CCCTCCACCC	GCGCGTCTCC	CCCCTTCTTT	60
TCCCCCTCTCC	GGAGGGGGGG	GAGGTGGGG	CGCGTGGGG	GGGTGGGGGG	TGGGGTGGC	120
GGGGGACCGC	CCCCGGCCGG	CAAAGGCCG	CCGCCGCGG	CACTTCAACC	GTAGCGGTGC	180
GCCCGCACCG	GCTACGAGAC	GGCTGGAAAG	GCCCGACGGG	GAATGTGGCT	CGGGGGGGGC	240
GGCGCGTCTC	AGGGCGCGCC	GAACCACTC	ACCCCGAGTG	TTACAGCCCT	CCGGCCGCGC	300
TTTCGCGGAA	TCCCCGGGGC	GAGGGGAAGC	CCGATAACCG	TCGCCGCGCT	TTTCCCCTCC	360
CCCCGTCCGC	CTCCC GGCG	GGCGTGGGG	TGGGGGCCGG	GCCGCCCTC	CCACGCCCGT	420
GGTTTCTCTC	TCTCCCGGTC	TCGGCCGGTT	TGGGGGGGGG	AGCCCGGTTG	GGGGCGGGGC	480
GGACTGTCT	CAGTGCACCC	CGGGCGTCGT	CGCGCCGTG	GGCCCGGGGG	GTTCTCTCGG	540
TCACGCCGCC	CCCCACGAAG	CCGAGCGCAC	GGGGTCGGCG	GCGATGTCGG	CTACCCACCC	600
GACCCGTCTT	GAAACACGGA	CCAAGGAGTC	TAACCGCGTGC	GCGAGTCAGG	GGCTCGCACG	660
AAAGCCGCCG	TGGCGCAATG	AAGGTGAAGG	GCCCCGTCCG	GGGGCCCGAG	GTGGGATCC	719

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGAGGCCTCT	CCAGTCCGCC	GAGGGCCAC	CACCGGCCCG	TCTCGCCCGC	CGCGTCGGGG	60
AGGTGGAGCA	CGAGCGTACG	CGTTAGGACC	CGAAAGATGG	TGAACATATGC	CTGGGCAGGG	120
CGAAGCCAGA	GGAAACTCTG	GTGGAGGTCC	GTAGCGGTCC	TGACGTGCAA	ATCGGTCGTC	180
CGACCTGGGT	ATAGGGCGA	AAGACTAATC	GAACCATCTA	GTAGCTGGTT	CCCTCCGAAG	240
TTTCCCTCAG	GATAGCTGGC	GCTCTCGCAA	CCTTCGGAAG	CAGTTTTATC	CGGGTAAAGG	300
CGGAATGGAT	TAGGAGGTCT	TGGGGCCCGA	AACGATCTCA	AACTATTCT	CAAACTTAA	360

ATGGGTAAGG	AAGCCCGGCT	CGCTGGCGTG	GAGCCGGCG	TGGAATGCGA	GTGCCTAGTG	420
GGCCACTTT	GGTAAGCAGA	ACTGGCGCTG	CGGGATGAAC	CGAACGCCGG	TTAAGGCAC	480
CCGATGCCGA	CGCTCATCAG	ACCCCAGAAA	AGGTGTTGGT	TGATATAGAC	AGCAGGACGG	540
TGGCCATGGA	AGTCGGAATC	CGCTAAGGAG	TGTGTAACAA	CTCACCTGCC	GAATCAACTA	600
GCCCTGAAA	TGGATGGCGC	TGGAGCGTCG	GGCCCATACC	CGGCCGTCGC	CGGCAGTCGG	660
AACGGGACGG	GACGGGAGCG	GCCGC				685

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGGAATTCC CCTATCCCTA ATCCAGATTG GTG 33

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAACTGCAGG CCGAGCCACC TCTCTCTGT GTTTG 35

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGGAATTCAC AGAAGAGAGG TGGCTCGGCC TGC 33

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:  
  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCCTGCAGG AAGTCATACC TGGGGAGGTG GCCC

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(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 80 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:  
  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAACTGCAGG TTAATTAACC CTAACCTAA CCCTAACCT AACCTAACCC CTAACCTAA  
CCCTAACCT AACCCGGGAT

60  
80

*A Cont*  
(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:  
  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTGGGCCCTA GGCTTAAGG

19

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:  
  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCCAGGGTTT TCCCAGTCAC GACGT

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(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 26 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Genomic DNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE:
  - (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTGCAAGGC GATTAAGTTG GGTAAC

26

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 26 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Genomic DNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE:
  - (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

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Cont*  
TATGTTGTGT GGAATTGTGA GCGGAT

26

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 21 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Genomic DNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE:
  - (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGGTTTAAAC AGATCTCTGC A

21